

Please amend the application as follows:

In the Specification

Replace the paragraph at page 15, lines 7 through 14 with the following paragraph:

Figure 19 depicts the amino acid sequence alignment of the core domain of ySir2 (SEQ ID NO: 14), yHST1 (SEQ ID NO: 15), yHST2 GenBank Accession NO: U39063, (SEQ ID NO: 16), yHST3 GenBank Accession No: U39062, (SEQ ID NO: 17), yHST4 GenBank Accession No: NC\_001136 (SEQ ID NO: 18), mSir2alpha (mSir2 $\alpha$ , SEQ ID NO: 19), mSir2beta (mSir2 $\beta$ , SEQ ID NO: 20), mSirg (mSir2 $\gamma$ , SEQ ID NO: 21), and deduced amino acid sequences of Sir2-like core domains (GenBank Accession No: AI465098, SEQ ID NO: 22; GenBank Accession No: AI465820, SEQ ID NO: 23; GenBank Accession No: AI466061, SEQ ID NO: 24).

Amendments to the specification are indicated in the attached "Marked Up Version of Amendments" (page i).

In the Claims

Amend Claim 1. Amendments to the claim are indicated in the attached "Marked Up Version of Amendments" (page i).

- D1  
C2
1. (Amended) A method of altering the acetylation status of at least one amino acid residue in a protein, the acetylation status consisting essentially of NAD-dependent acetylation status, by altering the activity of a Sir2 protein.

REMARKS

The remainder of this Reply and Preliminary Amendment is set forth under appropriate subheadings for the convenience of the Examiner.